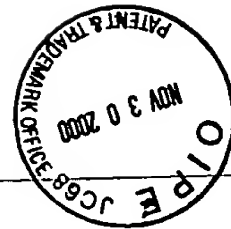


SEQUENCE LISTING



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DEC 08 2000

TECH CENTER 1600/2900

<110> Medical Research Council

Choo, Yen

Klug, Aaron

Isalan, Mark

<120> Nucleic Acid Binding Polypeptide Library

<130> 71278/264974

<140> US 09/424,482

<141> 1999-11-23

<150> GB9710809.6

<151> 1997-05-23

<150> PCT/GB98/01510

<151> 1998-05-25

<160> 19

<170> PatentIn version 3.0

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<223> 0 - 2 possible residues

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<223> 3 - 6 possible residues

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<222> (18)..(18)

<223> X is His or Cys

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Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Xaa Xaa
1 5 10 15

Xaa Xaa

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<223> Xaa is any amino acid

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<223> Xaa is any amino acid

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<223> 2 or 4 amino acids

<220>

<221> VARIANT

<222> (6)..(7)

<223> 2 or 3 amino acids

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Xaa Cys Xaa Xaa Cys Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa
1 5 10 15

His Xaa Xaa Xaa His
20

<210> 6

<211> 4

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Thr Gly Glu Lys
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Thr Gly Glu Lys Pro
1 5

<210> 8

<211> 26

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Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Lys Ser Asp
1 5 10 15

Leu Val Lys His Gln Arg Thr His Thr Gly
20 25

<210> 9

<211> 29

<212> PRT

<213> Artificial

<220>

<223> Description of Artificial Sequence: Consensus structure

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Pro Tyr Lys Cys Ser Glu Cys Gly Lys Ala Phe Ser Gln Lys Ser Asn
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Leu Thr Arg His Gln Arg Ile His Thr Gly Glu Lys Pro
20 25

<210> 10

<211> 6

<212> PRT

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Met Ala Glu Glu Lys Pro
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<210> 11

<211> 9

<212> DNA

<213> Artificial

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9

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sequenc

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9

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<212> DNA

<213> Artificial

<220>

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acgcccacg

9

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9

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<222> (7) .. (9)

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9

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Arg Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr
20 25 30

Gly Gln Lys Pro
35

<210> 17

<211> 28

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<222> (18)..(18)

<223> Xaa is any amino acid

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Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Asp Leu
1 5 10 15

Thr Xaa His Ile Arg Thr His Thr Gly Glu Lys Pro
20 25

<210> 18
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<222> (12)..(12)

<223> Xaa is any amino acid

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<222> (14)..(14)

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Phe	Ala	Cys	Asp	Ile	Cys	Gly	Arg	Lys	Phe	Ala	Xaa	Ser	Xaa	Asp	Arg
1				5				10						15	

Lys	Arg	His	Thr	Lys	Ile	His	Leu	Arg	Gln	Lys	Asp
			20				25				

<210> 19
<211> 28
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<222> (12)..(15)

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Phe	Ala	Cys	Asp	Ile	Cys	Gly	Arg	Lys	Phe	Ala	Xaa	Xaa	Xaa	Xaa	Arg
1				5				10						15	

Lys	Arg	His	Thr	Lys	Ile	His	Leu	Arg	Gln	Lys	Asp
			20				25				
